--BLAST analysis of known chemokine receptors identified a bovine receptor, PPR1, designated as a gustatory receptor (Matsuoka et al,., 1993, *Biochem Biophys Res Comm* 194:540-11). A search of a human EST database using the PPR1 sequence identified two non-contiguous EST's: H67224 and AI131555. Primers were designed against the 5' end of H67224 (5' AAT TTG GCT GTA GCA GAT TTA CTC C 3' [SEQ ID NO:4]) and in the reverse orientation for the 3' end of AI131555 (5' GCT AAA AGT ACT GGT TGG C 3'[SEQ ID NO:5]), and used in PCR (5% DMSO, annealing 58°C) of genomic DNA isolated from human buffy coats. The reaction resulted in a 855 bp product containing the ESTs and connecting sequences. The 855 bp fragment product was used to design additional primers for use in an anchored PCR screen of a Rapid Screen™ arrayed spleen cDNA library (Origene, Rockville, MD), yielding a 5' extended clone; this clone was finally used to screen a human genomic library by filter hybridization. Full length coding sequence was deduced by sequence analysis of genomic clones using reverse primer from the 5' sequence of Origene clone PCR with proofreading Pfu (Stratagene) enzyme. The refined sequence was confirmed on several clones and is shown in Figure 1. [A preliminary sequence determination differed from Figure 1 at the following positions: 47, 64, 78, 120, 131, 545, 571, 574 (using the numbering of Figure 1) which were G, G, G, C, C, T, A, and T, respectively [SEQ ID NO:3], which variant is also contemplated by the invention). The coding sequence was cloned into pIRESpuro expression vector (Clontech, Palo Alto, CA) with a FLAG epitope tag and prolactin signal sequence.--

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Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.

In the Claims:

Please amend claim 24 as follows:

24. A method of amplifying a CCX CKR polynucleotide in a sample comprising

(a) adding reagents sufficient for a polymerase chain reaction and at least two different primers to the sample, wherein each of said primers comprise at least 10 contiguous nucleotides identical or exactly complementary to SEQ ID NO:1; or,

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